

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 10:25:47 ; Search time 23 Seconds  
(without alignments)  
20.201 Million cell updates/sec

Title: US-09-756-899A-1  
Perfect score: 63  
Sequence: 1 AHSGHCCL 9

Scoring table: BLOSUM62  
Gapop 1G.0 , Gapext 0.5

Searched: 389414 seqs, 5162591 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : Issued Patents Aa:  
1: /cgn2\_5/ptodata/2/iaa/5A COMB.pep:  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:  
5: /cgn2\_-/ptodata/2/iaa/PCHTS\_COMB.pep:  
6: /cgn2\_6/ptodata/2/iaa/backflesi.pep:  
\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match	Length	DB	ID	Description
1	35	55.6	8	2	US-08-557-122A-24		Sequence 24, Appl
2	33	55.6	8	4	US-09-262-666-24		Sequence 24, Appl
3	33	52.4	6	1	US-08-068-395A-4		Sequence 4, Appl
4	33	52.4	6	1	US-08-464-365-4		Sequence 4, Appl
5	33	52.4	6	3	US-08-627-907A-5		Sequence 5, Appl
6	33	52.4	6	3	US-07-901-713A-1		Sequence 1, Appl
7	32	52.4	7	2	US-08-923-536A-5		Sequence 5, Appl
8	32	50.8	7	2	US-08-645-193B-65		Sequence 65, Appl
9	28	44.4	8	3	US-08-657-339A-12		Sequence 12, Appl
10	28	44.4	8	4	US-08-457-694A-12		Sequence 12, Appl
11	26	41.3	4	1	US-07-609-716-10		Sequence 10, Appl
12	26	41.3	4	1	US-08-477-509B-107		Sequence 107, APP
13	26	41.3	4	3	US-08-482-685B-107		Sequence 107, APP
14	26	41.3	4	3	US-08-475-411A-10		Sequence 10, Appl
15	26	41.3	4	3	US-08-478-029A-10		Sequence 10, Appl
16	26	41.3	4	4	US-08-444-791A-107		Sequence 107, APP
17	26	41.3	5	2	US-08-244-496-83		Sequence 83, Appl
18	26	41.3	7	2	US-08-923-536A-6		Sequence 6, Appl
19	26	41.3	9	3	US-09-259-754-368		Sequence 368, APP
20	26	41.3	9	3	US-09-042-107-368		Sequence 368, APP
21	26	41.3	9	4	US-09-722-250D-368		Sequence 368, APP
22	25	39.7	5	1	US-08-487-006-59		Sequence 59, Appl
23	25	39.7	6	2	US-08-488-659A-59		Sequence 59, Appl
24	25	39.7	6	4	US-09-058-740-6		Sequence 6, Appl
25	25	39.7	8	2	US-08-520-535-12		Sequence 12, Appl
26	25	39.7	8	2	US-09-079-432-12		Sequence 12, Appl
27	25	39.7	9	3	US-09-518-046-63		Sequence 63, Appl

**ALIGNMENTS**

RESULT 1  
US-08-557-122A-24

; Sequence 24, Application US/08557122A  
; Patent No. 5879664  
; GENERAL INFORMATION:  
; APPLICANT: Hiort, Carsten Mailand  
; TITLE OF INVENTION: Purified Protein Disulfide Isomerase  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5879664  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-1401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/557-122A  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J.  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 3980.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: peptide  
; US-08-557-122A-24  
; Query Match Score 35; DB 2;  
; Best Local Similarity 71.4%; Pred. No. 3e+05;  
; Matches 5; Conservative 0; Mismatches 2; Indels 0;  
; Gaps 0;  
Qy 1 AHWSGH 7  
Db 1 AFWCGHC 7

**RESULT 2**

US-09-262-666-24

Sequence 24 Application US/09262666  
Patent No. 6346244

GENERAL INFORMATION:

TITLE OF INVENTION: Fungal Protein Disulfide Isomerase

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6346244 No. 6346244 disk of No. 6346244th America, Inc.

STREET: 405 Lexington Avenue, 6th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/262,666

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/557,122

FILING DATE: 11-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 3980.204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-857-0123

TELEFAX: 212-78-9655

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLogy: single

STRANDEDNESS: single

MOLECULE TYPE: peptide

US-09-262-666-24

Query March

Best Local Similarity 71.4%; Pred. No. 3e+05;

Matches 5; Conservative 0; Mismatches 2; Indels 0;

Gaps 0;

Db 0;

Qy 1 AHWSGHC 7

Db 1 APWCGHC 7

RESULT 3

US-08-068-395A-4

Sequence 4 Application US/08068395A

Patent No. 5496719

GENERAL INFORMATION:

APPLICANT: YAMADA, YUKIO

APPLICANT: ASAMI, OSAKI

APPLICANT: SUGIYAMA, HIDEHIKO

APPLICANT: IDEKURA, CHIE

APPLICANT: HOSHINO, FUMIHIKO

APPLICANT: KIRAI, MASANA

APPLICANT: KAJINO, TSUTOMU

APPLICANT: IMAEDA, TAKAO

APPLICANT: SARAI, KIYOKO

APPLICANT: KAJINO, MASANA

APPLICANT: IMAEDA, TSUTOMU

APPLICANT: SARAI, KIYOKO

TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN DISULFIDE

ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR

PRODUCING THE SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &amp; NEUSTADT,

ADDRESSEE: P. C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/068,395A

FILING DATE: 19930527

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-135254

FILING DATE: 27-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-44013

FILING DATE: 04-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 549671man, F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 68-228-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELELEX: 244855 OPAT UR

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-068-395A-4

Query Match

Best Local Similarity 55.6%; Score 33; DB 1; Length 6;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 0;

Qy 3 WSGHC 7

Db 1 WCGHC 5

RESULT 4

US-08-464-365-4

Sequence 4 Application US/08464365

Patent No. 5700659

GENERAL INFORMATION:

APPLICANT: YAMADA, YUKIO

APPLICANT: ASAMI, OSAKI

APPLICANT: SUGIYAMA, HIDEHIKO

APPLICANT: IDEKURA, CHIE

APPLICANT: HOSHINO, FUMIHIKO

APPLICANT: KIRAI, MASANA

APPLICANT: KAJINO, TSUTOMU

APPLICANT: IMAEDA, TAKAO

APPLICANT: SARAI, KIYOKO

TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN DISULFIDE

ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR

PRODUCING THE SAME

NUMBER OF SEQUENCES: 10

TITLE OF INVENTION:

POLYPEPTIDE POSSESSING PROTEIN DISULFIDE

ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR

PRODUCING THE SAME

NUMBER OF SEQUENCES: 10

TITLE OF INVENTION:

POLYPEPTIDE POSSESSING PROTEIN DISULFIDE

ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR

PRODUCING THE SAME

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &amp; NEUSTADT,

ADDRESSEE: P. C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464,365  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 4-135254  
 FILING DATE: 27-MAY-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 5-44013  
 FILING DATE: 04-MAR-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 5-44014  
 FILING DATE: 04-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Olson, No. 570065mm F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 68-228-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 TELEX: 249855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 TOPOLogy: linear  
 MOLECULE TYPE: peptide  
 US-08-464-365-4

Query Match 52.4%; Score 33; DB 1; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 3e+05;  
 Matches 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

---

RESULT 5  
 US-08-227-907A-5  
 Sequence 5, Application US/08627907A  
 Patent No. 6060302  
 GENERAL INFORMATION:  
 APPLICANT: HIRANO, Naoto  
 TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA AND DNA  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: C/O FISH & NEAVE  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10020

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/627,907A  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 5-238402  
 FILING DATE: 24-SEP-1993  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/01572  
 FILING DATE: 22-SEP-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HALEY Jr., James P.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: SHGN-10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDBIORITY: not relevant  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: peptide  
 US-08-627-907A-5

Query Match 52.4%; Score 33; DB 3; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 3e+05;  
 Matches 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

---

RESULT 6  
 US-07-901-713A-1  
 Sequence 1, Application US/07901713A  
 GENERAL INFORMATION:  
 Patent No. 6291205  
 APPLICANT: Tuite, Michael F.  
 APPLICANT: Freedman, Robert B.  
 APPLICANT: Markus, Henry Z.  
 APPLICANT: Schnitz, Loren D.  
 APPLICANT: Montgomery, Donald W.  
 APPLICANT: Ellis, Ronald W.  
 TITLE OF INVENTION: METHOD FOR INCREASING PRODUCTION OF  
 TITLE OF INVENTION: DISULFIDE BONDED RECOMBINANT PROTEINS BY SACCAROMYCES  
 TITLE OF INVENTION: CERBYTISIAE  
 FILE REFERENCE: 18469  
 CURRENT APPLICATION NUMBER: US/07/901,713A  
 CURRENT FILING DATE: 1992-06-12  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FastSBQ for Windows Version 4.0  
 SEQ ID NO: 1  
 LENGTH: 6  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: vertebrate PDI active site  
 US-07-901-713A-1

Query Match 52.4%; Score 33; DB 3; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 3e+05;  
 Matches 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

---

RESULT 7  
 US-08-923-536A-5  
 Sequence 5, Application US/08923536A  
 Patent No. 5565426  
 GENERAL INFORMATION:  
 APPLICANT: SATAI, Yasuyoshi  
 APPLICANT: KATO, No. 595426uo  
 APPLICANT: SHIBANO, Yuji  
 TITLE OF INVENTION: PROTEIN DISULFIDE ISOMERASE GENE DERIVED  
 FROM STRAIN OF METHYLOTROPHIC YEAST  
 TITLE OF INVENTION:

NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BURNS, DOAN & MATHIS, L.L.P.  
 STREET: 1737 King Street, Suite 500  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22314-2756  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/923,536A  
 FILING DATE: 04-SEP-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 81-234287  
 FILING DATE: 04-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meath, Donna M.  
 REGISTRATION NUMBER: 36,607  
 REFERENCE/DOCKET NUMBER: 001560-317  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-6620  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Peptide  
 US-08-923-536A-5

Query Match 3 WSGHCC 8  
 Best Local Similarity 50.0%; Score: 32; DB: 2; Length: 7;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 DB 2 WNSYCC 7

RESULT 9  
 US-08-657-339A-12  
 Sequence 12, Application US/08657339A.  
 GENERAL INFORMATION:  
 PATENT NO. 6265531  
 APPLICANT: Duke-Cohan, Jonathan S.  
 ATTORNEY: Morimoto, Chikao  
 APPLICANT: Schlossman, Stuart F.  
 TITLE OF INVENTION: NOVEL FORM OF DIPEPTIDYLPEPTIDASE IV (CD26), FOUND IN  
 TITLE OF INVENTION: HUMAN SERUM, ANTIBODIES THERETO, AND USES THEREFOR  
 FILE REFERENCE: 00530-091001  
 CURRENT APPLICATION NUMBER: US/08/657,339A  
 CURRENT FILING DATE: 1996-06-03  
 PRIOR APPLICATION NUMBER: US 08/457,694  
 PRIOR FILING DATE: 1995-06-01  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 12  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-08-657-339A-12

Query Match 4 SGHCC 9  
 Best Local Similarity 66.7%; Score: 28; DB: 3; Length: 8;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 DB 1 SGHIC 6

RESULT 10  
 US-08-457-694A-12  
 Sequence 12, Application US/08457694A.  
 GENERAL INFORMATION:  
 PATENT NO. 6325599  
 APPLICANT: Duke-Cohan, Jonathan S.  
 ATTORNEY: Morimoto, Chikao  
 APPLICANT: Schlossman, Stuart F.  
 TITLE OF INVENTION: NOVEL FORM OF DIPEPTIDYLPEPTIDASE IV FOUND IN  
 FILE REFERENCE: 00530-090001  
 CURRENT APPLICATION NUMBER: US/08/457,694A  
 CURRENT FILING DATE: 1995-06-01  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 12



ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: US  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-It Release #1.0, Version #1.1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/482,085B  
 FILING DATE: 07-JUN-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 06/927,258  
 FILING DATE: 04-NOV-1986  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/114,618  
 FILING DATE: 29-OCT-1987  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/053,049  
 FILING DATE: 22-APR-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/175,155  
 FILING DATE: 29-DBC-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Trecatin, Richard F.  
 REGISTRATION NUMBER: 31,801  
 REFERENCE/DOCKET NUMBER: A 55186-6/RFT/MTK  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-781-1989  
 TELEFAX: 415-398-3249  
 INFORMATION FOR SEQ ID NO: 107:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 -08-482-085B-107  
 Query Match      Score 26; DB 3; Length 4  
 Best Local Similarity 100.0%; Pred. No. 3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0  
 /  
 6 HCC 8  
 |||  
 1 HCC 3  
 /  
 RESULT 14  
 -08-475-411A-10  
 Sequence 10, Application US/08475411A  
 Patent No. 6140072  
 GENERAL INFORMATION:  
 APPLICANT: ferrari, Franco A.  
 APPLICANT: Cappello, Joseph  
 TITLE OF INVENTION: Functional Recombinantly Prepared Synthetic Protein Polymer  
 TITLE OF INVENTION: Synthetic Protein Polymer  
 NUMBER OF SEQUENCES: 119  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/475,411A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,716  
 FILING DATE: 06-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/263,429  
 FILING DATE: 09-NOV-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/114,618  
 FILING DATE: 29-OCT-1987  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 06/927,258  
 FILING DATE: 04-NOV-1986  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Trecartin, Richard F.  
 REGISTRATION NUMBER: 31,801  
 REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-781-1989  
 TELEFAX: 415-398-3249  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide

S-08-475-411A-10

QUERY Match 41.3%; Score 26; DB 3; Len 10  
 Best Local Similarity 100.0%; Pred. No. 3e+05;  
 Matches 3; Conservative 0; Mismatches 0;

Y	6	HCC	8
b	1	HCC	3

RESULT 15  
 S-08-475-029A-10  
 Sequence 10. Application US/08478029A  
 Patent No. 6184348  
 GENERAL INFORMATION:  
 APPLICANT: Ferrati, Franco A.  
 APPLICANT: Cappello, Joseph  
 TITLE OF INVENTION: Functional Recombinantly Prepared Synthetic Protein Polymer  
 NUMBER OF SEQUENCES: 119  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Flehr, Rohbach, Test, Albritton & Heim  
 STREET: Four Bubaradero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/478,029A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,716  
 FILING DATE: 06-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/263,429

PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartis, Richard F.  
REGISTRATION NUMBER: 31,001  
TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: A-55186-8/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-38-3249  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-08-478-029A-10

Query Match Similarity 41.3%; Score 26; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qry 6 FCC 8  
Dib 1 FCC 3

Search completed: June 1, 2004, 10:29:22  
Job time : 24 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 10:25:46 ; Search time 21 seconds

(without alignments)  
41.225 Million cell updates/sec

Title: US-09-756-899A-1

Perfect score: 63

Sequence: 1 AHSSHCCCL 9

Scoring table: BiLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR\_78.\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
-	1	25	19.7	8	2	D61512	variant surface g1
	2	23	36.5	9	2	A60522	sperm-activating p
	3	21	33.3	8	2	C61512	variant surface g1
	4	18	28.6	6	2	PT0652	T-cell receptor be
	5	18	28.6	6	4	179566	hypothetical TCL3
	6	18	28.6	8	2	PC1002	leucine-tRNA ligas
	7	18	28.6	9	2	QDRB	deinucleic acid
	8	18	28.6	9	2	A43848	cell surface adhes
	9	18	28.6	9	2	PT0562	T-cell receptor be
	10	18	28.6	9	2	PH0942	T-cell receptor be
	11	17	27.0	4	2	B53284	hypothetical prote
	12	17	27.0	7	2	S08602	T-cell receptor be
	13	17	27.0	7	2	PT0642	T-cell receptor be
	14	17	27.0	7	2	PT0586	T-cell receptor be
	15	17	27.0	7	2	PT0728	T-cell receptor be
	16	17	27.0	8	2	A25816	L-serine ammonia
	17	17	27.0	9	2	A12872	transaldolase (EC
	18	17	27.0	9	2	A11497	T-cell receptor be
	19	17	27.0	9	2	PT0634	Ig heavy chain CRD
	20	16	25.4	5	2	PT0281	litterin 2-Glu - Au
	21	15.5	24.6	9	2	S07205	litterin I - Australia
	22	15.5	24.6	9	2	S07204	litterin - Rohde's
	23	15	24.6	9	2	S07241	T-cell receptor be
	24	15	23.8	4	2	PT0661	actin I - malaria
	25	15	23.8	5	2	B45525	Ig heavy chain CDR
	26	15	23.8	9	2	PT0231	macrophage chemotact
	27	15	23.8	9	2	A37027	growth-modulating
	28	14	22.2	3	3	GKHU	carbon monoxide de
	29	14	22.2	4	2	PL0140	probable manipuly

#### RESULT 1

D61512

variant surface glycoprotein MITat 1.6 - Trypanosoma brucei (fragment)

C.Species: Trypanosoma brucei

C.Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-May-1999

C.Accession: D61512

R.Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A.Title: Glycoproteins from variant surface glycoproteins of Trypanosoma brucei. C-term

A.Reference number: A61512; PMID:81172836; PMID:6163983

A.Status: Preliminary

A.Molecule type: protein

A.Residues: 1-8 <RQL>

C.Keywords: glycoprotein

Query Match

Best Local Similarity

Matches 3;

Conservative

0;

Mismatches 3;

Indels 0;

Gaps 0;

Qy 3 WSGHC 8

Db 1 WEGETC 6

#### RESULT 2

A60522

spem-activating peptide SAP-IV - sea urchin (Diadema setosum)

C.Species: Diadema setosum

C.Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000

C.Accession: A60522

R.Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzuki, Comp. Biochem. Physiol. B 95, 423-429, 1990

A.Title: A species-specific sperm-activating peptide from the egg jelly of the sea urchin

A.Reference number: A60522; PMID:90227916; PMID:2158412

A.Accession: A60522

A.Molecule type: protein

A.Residues: 1-9 <YOS>

C.Superfamily: unassigned animal peptides

F7-9/disulfide bonds: #stacutus experimental

Query Match

Best Local Similarity

Matches 3;

Conservative

0;

Mismatches 3;

Indels 0;

Gaps 0;

Qy 3 WSGHC 8

Db 4 WGEAVC 9

RESULT 3

C61512

variant surface glycoprotein MIRat 1.4 - Trypanosoma brucei (fragment)

RESULT 6  
C:Species: Trypanosoma brucei  
C:Accession: C61512  
C:Status: Preliminary  
R:Holder: A.A.; Cross, G.A.M.  
Mol: Biochem Parasitol 2, 135-150, 1981  
A;Title: Glycopeptides from variant surface Glycoproteins of Trypanosoma brucei. C-terminal  
A;Reference number: A61512; MUID:6163983; PMID:81172836;  
A;Accession: C61512  
A;Molecule type: protein  
A;Residues: 1-8 <HOL>  
C;Keywords: glycoprotein

Query Match 33.3%; Score 21; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Indels 0; Gaps 0;  
QY 3 WSGHCC 8  
Db 1 WENNAC 6

RESULT 4  
PT0652  
T-cell receptor beta chain V-D-J region (121-1E) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Accession: PT0652  
C;Status: sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
J. Bxp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0650; MUID:91277601; PMID:1711558  
A;Accession: PT0652  
A;Status: translation not shown  
A;Molecule type: tRNA  
A;Residues: 1-6 <PEE>  
A;Experimental source: day 4 postnatal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 28.6%; Score 18; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Indels 0; Gaps 0;  
QY 4 SGHC 7  
Db 2 SGDC 5

RESULT 5  
hypothetical tcl3 protein (mistranslated) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Accession: I79564  
R: Zurter, M.; Hockert, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.C.; Proc. Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990  
A;Title: The t(10;14) (q22;q11) of T-cell acute lymphoblastic leukemia juxtaposes the delta  
A;Reference number: I59162; MUID:90222189; PMID:2326224  
A;Accession: I79564  
A;Status: translation not shown; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-6 <ZUT>  
A;Cross-references: GB:M33602; NID:9339907; PID:9807656  
C;Comment: This is the hypothetical translation of a sequence translated in an incorrect

Query Match 28.6%; Score 18; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Indels 0; Gaps 0;

QY 7 CC 8  
Db 3 CC 4

RESULT 7  
QDRB  
delta sleep-inducing peptide - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Accession: A01422  
R;Monnier, M.; Dudler, L.; Gaither, R.; Maier, P.F.; Tobler, H.J.; Schoenberger, G.A.  
Exp. Neurol. 33, 548-552, 1977  
A;Title: The delta sleep inducing Peptide (DSIP). Comparative properties of the original  
A;Reference number: A01422; MUID:77185344; PMID:562769  
A;Accession: A01422  
A;Molecule type: protein  
A;Residues: 1-9 <MON>  
C;Comment: This peptide was obtained from dialysates of occipital venous sinus blood of recipient rabbits, it induces spindle and delta EEG activity and reduced motor activity  
C;Superfamily: unassigned animal peptides

Query Match 28.6%; Score 18; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Indels 0; Gaps 0;

QY 7 CC 8  
Db 4 CC 5

RESULT 8  
A43848  
cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)  
C;Species: Staphylococcus aureus  
C;Accession: A43848  
R;Liang, D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.  
Infect. Immun. 60, 899-906, 1992  
A;Title: Binding of heparan sulfate to Staphylococcus aureus.  
A;Reference number: A43848; MUID:9217605; PMID:1511563  
A;Accession: A43848  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <IIA>  
A;Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 28.6%; Score 18; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

QY 7 CC 8  
Db 3 CC 4

NCBI-BLASTN search results for T-cell receptor beta chains.

**RESULT 9**

Query: PT0562  
T-cell receptor beta chain V-D-J region (126-1AK) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

R;Feeney, A.J.  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference: PT0562

A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-9 <FEES>  
A;Experimental source: day 18 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSG 5  
1:1  
Db 2 WTG 4

**RESULT 10**

Query: PH0942  
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

;Accession: PH0942

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandienbart, A.A.; Wilson, D.B.  
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis. J. Exp. Med. 174, 1467-1476, 1991

A;Reference: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0942

A;Molecule type: mRNA  
A;Residues: 1-9 <GOL>  
A;Experimental source: complete Freund's adjuvant-immunized lymph node  
A;Note: the authors translated the codon TGC for residue 2 as Ala  
C;Keywords: T-cell receptor

Query Match 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HKSG 5  
1:1  
Db 6 NWGG 9

**RESULT 11**

Query: B53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

R;Ranbiranathan, N.; Alexander, C.B.; Mage, R.G.  
Mol Immunol. 28, 881-888, 1991

A;Title: Evolutionarily conserved organization and sequences of germline diversity and gene conversion in the T-cell receptor beta 2 chain D region. Mol Immunol. 28, 881-888, 1991

A;Reference: A53284; MUID:91342695; PMID:1678859

A;Accession: B53284

A;Status: preliminary  
A;Residues: 1-4 <DNA>

Query Match 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSG 5  
1:1  
Db 5 WGG 7

**RESULT 12**

Query: S08606  
Hypothetical protein 2 estrogen receptor 5'-region - chicken

C;Species: Gallus gallus (chicken)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 18-Aug-2000

;Accession: S08606

R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, B.; Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, B.; Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, B.; Title: The chicken oestrogen receptor sequence: homology with v-erbA and the h-ras oncogene. Mol Cell Biol. 10, 273-282, 1990

A;Reference number: S07192; MUID:86247578; PMID:3755102

A;Accession: S08606

A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <KRUS>  
A;Cross-references: EMBL:X03805; NID:963378; PIDN:CAA27432.1; PMID:9584490

C;Superfamily: unassigned leader peptides

Query Match 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HC 7  
1:1  
Db 5 HC 6

**RESULT 13**

Query: PT0642  
T-cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

;Accession: PT0642

R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0642

A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <FEES>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSG 5  
1:1  
Db 5 WGG 7

**RESULT 14**

Query: PT0586  
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0586  
 A;Status: translation not shown  
 A;Molecule type: tRNA  
 A;Residues: 1-7 <PFB>  
 A;Experimental source: day 19 fetal thymus, strain BAUB/c (clones 141-1CN and 141-1CD)  
 C;Keywords: T-cell receptor

Query Matchn Score 17; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 WSG 5  
     |  
 Db 5 WGG 7

---

RESULT 15  
 PT0728  
 T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0728  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0728  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-7 <PFB>  
 A;Experimental source: newborn thymus, strain BAUB/C  
 C;Keywords: T-cell receptor

Query Matchn Score 17; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 WSG 5  
     |  
 Db 5 WGG 7

Search completed: June 1, 2004, 10:28:46  
 Job time : 22 secs



ID	TAL1_PICJA	STANDARD;	PRT;	9 AA.	
AC	P17440;				
DT	01-AUG-1990 (Rel. 15, Created)				
DT	02-AUG-1990 (Rel. 15, Last sequence update)				
DT	28-FEB-2003 (Rel. 1, Last annotation update)				
DB	Transaldolase I (EC 2.2.1.2) (Fragment);				
DB	Pichia jadinii (Yeast) (Candida utilis);				
OS	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Pichia; Saccharomycetaceae; Saccharomycetidae; Pichia.				
OC	NCBI_TaxID=4903;				
OX	NCBI_TaxID=4903;				
RN	SEQUENCE;				
RX	MEDLINE=77110646; PubMed=556924;				
RA	Sun S.C.; Joris L.; Tsolias O.; RT				
RT	"Purification of crystallization of transaldolase isozyme I and evidence for different genetic origin of isozymes I and III in Candida utilis";				
RL	Arch. Biochem. Biophys. 178:69-78 (1977).				
CC	-!- FUNCTION: Transaldolase is important for the balance of metabolites in the pentose-phosphate pathway.				
CC	-!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.				
CC	-!- PATHWAY: Pentose phosphate pathway; nonoxidative part.				
CC	-!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.				
DR	PIR: A12872; A12872;				
DR	InterPro; IPR001598; Transaldolase.				
DR	PROSITE; PS00958; TRANSLDOLASE_2; PARTIAL.				
DR	PROSITE; PS01054; TRANSLDOLASE_1; PARTIAL.				
DR	Transferase; Pentose shunt.				
FT	NON TER 1 1				
FT	NON TER 9 9				
SQ	SEQUENCE 9 AA; 1008 MW; 274F31AF0EB1B058 CRC64;				
Query Match	27.0%; Score 17; DB 1; Length 9;				
Best Local Similarity	100.0%; Pred. No. 1.4e+05;				
Matches	2; Conservative 0; Mismatches 0;				
Indels	0; Gaps 0;				
Qy	6 HC 7				
Db	4 HC 5				
RESULT 3					
TAL3_PICJA	STANDARD;	PRT;	9 AA.		
AC	P17441;				
DT	01-AUG-1990 (Rel. 15, Created)				
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	28-FEB-2003 (Rel. 1, Last annotation update)				
DE	Transaldolase III (EC 2.2.1.2) (Fragment).				
OS	Pichia jadinii (Yeast) (Candida utilis);				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Saccharomycetales; Saccharomycetidae; Pichia.				
OX	NCBI_TaxID=4903;				
RN	SEQUENCE;				
RX	MEDLINE=75145197; PubMed=1092268;				
RA	Tsolias O.; Sun S.C.; RT				
RT	"Isolation of a Peptide containing a histidinyl-cysteinyl sequence from the active center of transaldolase";				
RL	Arch. Biochem. Biophys. 167:1525-1533 (1975).				
CC	-!- FUNCTION: Transaldolase is important for the balance of metabolites in the pentose-phosphate pathway.				
CC	-!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.				
CC	-!- PATHWAY: Pentose phosphate pathway; nonoxidative part.				
CC	-!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.				
DR	PIR: A11497; A11497.				
DR	InterPro; IPK001565; Transaldolase.				
DR	PROSITE; PS00958; TRANSLDOLASE_2; PARTIAL.				
DR	PROSITE; PS01054; TRANSLDOLASE_1; PARTIAL.				
FT	NON TER 1				
FT	NON TER 9 AA; 1091 MW; 8D38676323676BBA_CRC64;				
Query Match	25.4%; Score 16; DB 1; Length 9;				
Best Local Similarity	40.0%; Pred. No. 1.4e+05;				
Matches	2; Conservative 0; Mismatches 3;				
Indels	0; Gaps 0;				
Qy	3 WSGHC 7				
Db	5 WKPMC 9				
RESULT 5					
LIT0_LITAU	STANDARD;	PRT;	9 AA.		
ID	LIT0_LITAU				
AC	P0845;				
DT	01-NOV-1998 (Rel. 09, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				

DT 10-OCT-2003 (Rel. 42; Last annotation update)

DS Litoria aurea (Green and Golden bell frog).

QS Litoria aurea; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyliidae;

CC pelodryadinae; Litoria.

NCBI TaxID=8371;

RN [1]

RP SEQUENCE.

RC TISSUE-Skin secretion;

RX MEDLINE=75187011; PubMed=1140241;

RA Anastassi A., Braspamer V., Endean R.;

RT Aminocid peptide sequence of litorin, a bombesin-like nonapeptide from the skin of the Australian leptodactylid frog Litoria aurea.

RL Experientia 31:510-511(1975).

RN [2]

RP SEQUENCE, AND METHYLATION OF GLN-2.

RC TISSUE-Skin secretion;

RX MEDLINE=78003546; PubMed=980337;

RA Anastassi A., Montecucci P.C., Angelucci F., Braspamer V., Endean R.;

RT "Glu(One)3-litorin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea.";

RL Experiments 33:1289-1289(1977).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin Family.

DR PIR; S07204; S07205; S07206; S07207; S07208; S07209; S07210; DR InterPro; IPRE00074; Bombesin.

DR PROSITE; PS00237; BOMBESIN; 1.

KW Amphibian defense Peptides; Bombesin family; Amidation; Methylation;

PT Pyrolylone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID. AMIDATION AND METHYLATION (PARTIAL).

FT MOD RES 2 2 DEAMIDATION.

FT MOD RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 1103 MW; D7CCC1EB8628DC366 CRC64;

Query Match 24 6%; Score 15.5; DB 1; Length 9; Best Local Similarity 60.0%; Pred. No. 1.4e+05; Matches 3; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 3 WS-GH 6

Db 3 WAGH 7

CC Family.

DR PIR; S07241; S07241; Bombesin.

DR InterPro; IPR000374; Bombesin.

DR Pfam; PF0044; Bombesin; 1.

DR PROSITE; PS00237; BOMBESIN; 1.

KW Amphibian defense peptide; Bombesin family; Amidation;

PT Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID. AMIDATION.

SQ SEQUENCE 9 AA; 1090 MW; 4ECCC1EB861ADC377 CRC64;

Query Match 24 6%; Score 15.5; DB 1; Length 9; Best Local Similarity 60.0%; Pred. No. 1.4e+05; Matches 3; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 3 WS-GH 6

Db 3 WAGH 7

---

RESULT 7

UP001\_MOUSE

ID UP001\_MOUSE STANDARD; PRT; 5 AA.

AC P38639;

DT 01-OCT-1994 (Rel. 30; Created)

DT 01-OCT-1994 (Rel. 30; Last sequence update)

DT 15-MAR-2004 (Rel. 43; Last annotation update)

DR Unknown protein from 2D-page of fibroblasts (P19) (Fragment).

OS Mus musculus (Mouse).

OC Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Rodentia; Sciurognathia; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE.

RC TISSUE=FBroblast; PMID=7523108;

RA Merrick B.A., Patterson R.M.; Wichter L.L.; He C., Selkirk J.K.;

RA RT Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.,";

RA Electrophoresis 15:735-745(1994);

CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is 6.6, its MW is: 19 kDa.

CC NON TER 5

SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 23 8%; Score 15; DB 1; Length 5; Best Local Similarity 66.7%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSG 5

Db 1 WIG 3

---

RESULT 8

NEF\_HV128

ID NEF\_HV128 STANDARD; PRT; 9 AA.

AC P12381;

DT 01-OCT-1989 (Rel. 12; Created)

DT 01-OCT-1989 (Rel. 12; Last sequence update)

DT 10-OCT-2003 (Rel. 42; Last annotation update)

DR Negative factor (P-protein) (27 kDa protein) (3'ORF) (Fragment).

NCBI\_TaxID=11681;

OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).

OC Viruses; Retroviridae; Lentivirus.

NCBI\_TaxID=11681;

RP SEQUENCE FROM N.A.

RC TISSUE=Skin secretion;

RX MEDLINE=85127560; PubMed=3838283;

RA Barra D., Braspamer G.F., Siamaco M., Bossa F., Melchiorri P.,

RA Braspamer V.;

RT "Rohde's leaf frog: a new peptide from the skin of Phyllomedusa rohdei.";

RL FEBS Lett. 182:53-56(1985).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin isolate of HIV-1."

RL	AIDS Res. Hum. Retroviruses 4:165-173 (1988).	
CC	-!- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating activities. It seems to down-regulate the CD4 (T4) antigen.	
CC	-!- MISCELLANEOUS: THE 2'-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD ZAIRIAN MALE.	
CC		
CC	This SWISS-PROT entry is copyright of Bioinformatics and the KMBL outstation - between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC		
DR	EMBL; J03853; AAA44687.1; -	
DR	HIV; J03655; NBF5JYI.	
KW	AIDS; Myristate; GTP-binding; Lipoprotein.	
FT	LIPID 2 N-myristoyl glycine (in host) (By similarity).	
PT	NON TER 9 9 MW: 3190CB32A3733B78 CRC64;	
SQ	SEQUENCE 9 AA: 967 MW:	
	Query Match 23.8%; Score 15; DB 1; Length 9;	
	Best Local Similarity 100.0%; Pred. No. 1.4e+05;	
	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	3 WS 4	
Db	5 WS 6	
	2 GH 3	
RESULT 9		
ID	GRMM_HUMAN STANDARD: PRT; 3 AA.	
AC	P01157;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	21-JUL-1986 (Rel. 01, Last annotation update)	
DE	Growth-modulating peptide.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	SEQUENCEID=77162369; PubMed=8583556;	
RX	Schlesinger D.H.; Pickhart L.; Thaler M.M.;	
RT	"Growth-modulating serum tripeptide is glycyl-histidyl-lysine."	
RU	Experientia 33:32-35(1977).	
CC	-!- MISCELLANEOUS: This serum tripeptide has been found to stimulate growth of some cell types and to inhibit other types in vitro.	
DR	GO: GO:0001558; F: regulation of cell growth; NAS.	
SQ	SEQUENCE 3 AA: 340 MW: 6331EB8100000000 CRC64;	
Query Match 22.2%; Score 14; DB 1; Length 3;		
Best Local Similarity 100.0%; Pred. No. 1.4e+05;		
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	5 GH 6	
Db	1 GH 2	
RESULT 9		
ID	GRMM_HUMAN STANDARD: PRT; 3 AA.	
AC	P01157;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	21-JUL-1986 (Rel. 01, Last annotation update)	
DE	Growth-modulating peptide.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	SEQUENCEID=77162369; PubMed=8583556;	
RX	Schlesinger D.H.; Pickhart L.; Thaler M.M.;	
RT	"Growth-modulating serum tripeptide is glycyl-histidyl-lysine."	
RU	Experientia 33:32-35(1977).	
CC	-!- MISCELLANEOUS: This serum tripeptide has been found to stimulate growth of some cell types and to inhibit other types in vitro.	
DR	GO: GO:0001558; F: regulation of cell growth; NAS.	
SQ	SEQUENCE 3 AA: 340 MW: 6331EB8100000000 CRC64;	
Query Match 22.2%; Score 14; DB 1; Length 3;		
Best Local Similarity 100.0%; Pred. No. 1.4e+05;		
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	5 GH 6	
Db	1 GH 2	
RESULT 10		
ID	DGM1_PSECH STANDARD: PRT; 4 AA.	
DCML_PSECH		
AC	P19916;	
DT	01-FEB-1991 (Rel. 17, Created)	
DT	01-FEB-1991 (Rel. 17, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO	
DE	dehydrogenase subunit L) (CO-DH L) (Fragment).	
GN	CUTL.	
RP	SEQUENCE.	
RX	Kraut M.; Rüsgendieck I.; Herwig S.; Meyer O.;	
RA	"Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria."	
RT	Arch. Microbiol. 152:335-341(1989).	
RL	-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.	
CC	-!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced acceptor.	
CC	-!- COFACTOR: Molybdenum (molybdopterin).	
CC	-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.	
DR	PIR; PI0140; PI0140.	
KW	Oxidoreductase; Molybdenum.	
FT	NON_TER 4 4 MW: 7761EB76F0000000 CRC64;	
SQ	SEQUENCE 4 AA: 441 MW:	
	Query Match 22.2%; Score 14; DB 1; Length 4;	
	Best Local Similarity 100.0%; Pred. No. 1.4e+05;	
	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	5 GH 6	
Db	2 GH 3	
RESULT 11		
ID	MOSH_CLYJA STANDARD: PRT; 9 AA.	
AC	P19852;	
DT	01-FEB-1991 (Rel. 17, Created)	
DT	01-FEB-1991 (Rel. 17, last sequence update)	
DT	10-OCT-2003 (Rel. 42, last annotation update)	
DE	Spemann-activating peptide SAP-b ([His8]-mosact).	
OS	Clypeaster japonicus (sand dollar).	
OC	Eukaryota; Metazoa; Echinodermata; Eeltherozoa; Echinoozoa;	
OC	Echinoidea; Euechinoidea; Gnathostomata; Clypeasterida;	
CC	Clypeasteridae; Clypeaster.	
OX	NCBI_TaxID=7644;	
RN	SEQUENCEID=1116743; PubMed=2076468;	
RP	Tissue=Egg jelly;	
RC	Takao T.; Yoshino K.; Suzuki N.; Kajiura H.; Nomura K.,	
RA	Suzuki N.; Kurita M.; Yoshino K.I.; Kajiura H.; Nomura K.,	
RA	Yamaguchi M.;	
RA	"Purification and structure of mosact and its derivatives from the egg jelly of the sea urchin Clypeaster japonicus."	
RT	Zool. Sci. 4:649-656 (1987).	
RN	[2]	
RP	BROMINATION OF HIS-6.	
RC	MEDLINE=9116743; PubMed=2076468;	
RA	Takao T.; Yoshino K.; Suzuki N.; Shimonishi Y.;	
RA	Analysis of post-bombardment modifications of proteins by accurate mass measurement in fast atom bombardment mass spectrometry.;	
RT	Biomed. Environ. Mass Spectrom. 19:705-712(1990).	
PL	-!- FUNCTION: Stimulates sperm respiration and motility.	
CC	DR PIR; JN0026; JN0026.	
RN	Bromination.	
FT	MOD_RES 6 6 BROMINATION (PARTIAL).	
SQ	SEQUENCE 9 AA: 914 MW:	
	Query Match 22.2%; Score 14; DB 1; Length 9;	
	Best Local Similarity 60.0%; Pred. No. 1.4e+05;	
	Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 AHWSG 5	
Db	5 AHLTG 9	



RA Delage M.; Schooley D.A.;  
RT "Identification of an arginine vasopressin-like diuretic hormone from  
Locusta migratoria.",  
RL Biochem. Biophys. Res. Commun. 149:180-186 (1987).  
CC -!- FUNCTION: DIURETIC HORMONE.  
-!- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.  
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.  
DR PIR: A29477; A29477.  
DR Inter-Pro: IPR000981; Neurhyp\_horm.  
DR Pfam: PF00220; Hormone4; 1.  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
DR Hormone: Neuropeptide: Amidation.  
KW DISULFID IN F1.  
FT DISULFID 1 6 INTERCHAIN (WITH C-6) (IN F2).  
FT DISULFID 1 1 INTERCHAIN (WITH C-1) (IN F2).  
FT DISULFID 6 6 AMIDATION.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 20.6%; Score 13; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 CL 9  
Db |||  
1 CL 2

Search completed: June 1, 2004, 10:27:20  
Job time : 13 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: June 1, 2004, 10:25:46 ; Search time 39 Seconds  
(without alignments)  
72.812 Million cell updates/sec

Title: US-09-756-899a-1

Perfect score: 63

Sequence: 1 AHWSGHCLL 9

Scoring table: BLOSUM62  
GapOp 10.0 , GapExt 0.5

Searched: 101041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-Processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
1: sg_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rabbit:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_tvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2	34.9	9 10	Q9FSZ2		Q9FSZ2 cicer arietinum
2	19.5	31.0	8 6	Q02631		Q02631 orctolagus
3	19	30.2	8 4	Q8IVB7		Q8IVB7 homo sapien
4	19	28.6	9 8	Q8W8X4		Q8W8X4 diaedema mexicanum
5	18	28.6	8 13	Q9BTUS		Q9BTUS xenopus laevis
6	18	28.6	9 2	Q9R5M1		Q9R5M1 staphylococcus aureus
7	18	28.6	9 11	Q08979		Q08979 mus musculus
8	18	28.6	9 12	Q9BIU7		Q9BIU7 hepatitis b virus
9	17	27.0	8 4	Q15900		Q15900 homo sapien
10	17	27.0	9 4	Q99BB7		Q99BB7 homo sapien
11	17	27.0	9 15	Q85723		Q85723 simian sarcocystis
12	16	25.4	9 8	Q94NBL1		Q94NBL1 microcephalus
13	16	25.4	9 8	Q94NB2		Q94NB2 microcephalus
14	16	25.4	9 8	Q94NA9		Q94NA9 daubentonii
15	16	25.4	9 8	Q94XE6		Q94XE6 tectocoris
16	16	25.4	9 8	Q94NBO		Q94NBO microcephalus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2	34.9	9 10	Q9FSZ2		Q9FSZ2 cicer arietinum
2	19.5	31.0	8 6	Q02631		Q02631 orctolagus
3	19	30.2	8 4	Q8IVB7		Q8IVB7 homo sapien
4	19	28.6	9 8	Q8W8X4		Q8W8X4 diaedema mexicanum
5	18	28.6	8 13	Q9BTUS		Q9BTUS xenopus laevis
6	18	28.6	9 2	Q9R5M1		Q9R5M1 staphylococcus aureus
7	18	28.6	9 11	Q08979		Q08979 mus musculus
8	18	28.6	9 12	Q9BIU7		Q9BIU7 hepatitis b virus
9	17	27.0	8 4	Q15900		Q15900 homo sapien
10	17	27.0	9 4	Q99BB7		Q99BB7 homo sapien
11	17	27.0	9 15	Q85723		Q85723 simian sarcocystis
12	16	25.4	9 8	Q94NBL1		Q94NBL1 microcephalus
13	16	25.4	9 8	Q94NB2		Q94NB2 microcephalus
14	16	25.4	9 8	Q94NA9		Q94NA9 daubentonii
15	16	25.4	9 8	Q94XE6		Q94XE6 tectocoris
16	16	25.4	9 8	Q94NBO		Q94NBO microcephalus

9	8	Q95db8	lepilemur e
		Q85db0	lepilemur s
		Q58888	homo sapien
		Q4vvc1	varanus ruficauda
		Q9tdd0	titanotarsus
		Q94px5	felis silvestris
		Q9avb2	varanus salvator
		Q9apx7	felis silvestris
		Q94px6	felis libycus
		Q9avb5	varanus sahyadrensis
		Q9avc6	varanus salvator
		Q9prj4	lepisosteus osseus
		Q82445	nicotiana tabacum
		Q9ry3	sus scrofa
		Q15999	homo sapiens
		Q89491	murine leukemia virus
		Q66113	cherry leaf spot virus
		Q94564	cinnamomum zeylanicum
		Q85406	coixia buettneri
		Q47663	escherichia coli
		Q9UNP3	homo sapiens
		Q61723	mus musculus

## ALIGNMENTS

RESULT 1	Q9FSZ2	ID	PRELIMINARY;	PRT;	9 AA.
	Q9FSZ2	ID	Q9FSZ2;		
		AC	Q9FSZ2;		
		DT	01-MAR-2001 (TREMBLrel. 16, Created)		
		DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
		DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
		DB	Hypothetical protein (Fragment).		
		OS	Cicer arietinum (Chickpea) (Garbanzo).		
		OC	Bukaryota; Viridiplantae; Streptophytina; Embryophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids; euuroids I; Fabales; Fabaceae; Papilioideae; Cicereae; Cicer.		
		DR	EMBL: AU2293059; CAC10216.1; NCBI: TAXID=38227; [1] --		
		RN	SEQUENCE FROM N.A.		
		RC	STRAIN=cv. Castellana; TISSUE=Btiolated epicotyl;		
		RA	Dopico B.; Jimenez T.; Labrador E.; RT "cDNA clones expressed in etiolated Cicer arietinum epicotyls."		
		RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.		
		DR	EMBL: AU2293059; CAC10216.1; NCBI: TAXID=38227; KW HYPOTHETICAL PROTEIN.		
		FT	NON_TER	1	1
		FT	SEQUENCE	9 AA;	990 MW;
		FT			9441BDDAA7272EBB CRC64;

Query Match	34.9%	Score 22;	DB 10;	Length 9;
Best Local Matches	100.0%	Pred. No. 1e+06;	Indels 0;	Gaps 0;
3	Conservative	0;	Mismatches 0;	
2	Matches	0;		
1				
QY	7 CCL 9			
	2 CCL 4			
Db				

RESULT 2

002831 PRELIMINARY; PRT; 8 AA.

002831 AC 002831; Created

002831 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

002831 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Pro alpha 1 type III collagen protein (Fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX NCBI\_TaxID=9986;  
RN SEQUENCE FROM N.A.  
RX MEDLINE#=9637739; PubMed=878186;  
RA Metsaranta M.; Kujala U.M.; Pelliniemi L.; Osterman H.; Aho H.,  
RA Vuorio E.;  
RT "Evidence for insufficient chondrocytic differentiation during repair  
of full-thickness defects of articular cartilage.";  
RL Matrix Biol. 15:39-47 (1996).  
DR EMBL: S83371; AAD14433.1; -.  
KW Collagen.  
FT NON TER 1 102B MW; B859C7272EA77371 CRC64;  
SQ SEQUENCE 8 AA; 102B MW; B859C7272EA77371 CRC64;  
Query Match 31.0%; Score 19.5; DB 6; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 3; Gaps 1;  
Qy 2 HWSGHCCCL 9  
Db 1 HWP---CL 5

RESULT 3  
ID Q8IV87 PRELIMINARY; PRT; 8 AA.  
AC Q8IV87;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-JUN-2003 (TrEMBLrel. 23, Last sequence update)  
DE DJ107712.2 (Serine Palmitoyltransferase, long chain base subunit  
2-like (Amnion transferase 2), variant 1) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN SEQUENCE FROM N.A.  
RA Smith M.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
DR GO:0015740; F:transferase activity; IEA.  
KW Transferase.  
FT NON TER 1 1  
SQ SEQUENCE 8 AA; 908 MW; B8533682CEBBB042 CRC64;

Query Match 30.2%; Score 19; DB 4; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
ID Q8W8X4 PRELIMINARY; PRT; 9 AA.  
AC Q8W8X4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DB Cytochrome oxidase subunit II (Fragment).  
GN Diadema mexicanum.  
OS Diadema mexicanum.  
OC Mitochondrion.  
OU Eukaryota; Metazoa; Echinodermata; Blastozoa; Echinozoa;

OC Echinoidea; Euechinoidea; Diadematida; Diadematoida; Diadematidae;  
OC Diadema.  
NCBI\_TaxID=105359;  
OX N.A.  
RN SEQUENCE FROM N.A.  
RC STRAIN=CC70, and CC117;  
RX MEDLINE#=21123357; PubMed=11430656;  
RA Lessios H.A.; Kessing B.D.; Pearse J.S.;  
RT "Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema.";  
RL Evolution 55:955-975 (2001).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CC70, and CC117;  
RX MEDLINE#=21561594; PubMed=11703875;  
RA Lessios H.A.; Garrido M.J.; Kessing S.D.;  
RT "Demographic history of Diadema antillarum, a keystone herbivore on Caribbean reefs";  
RL Proc. R. Soc. Lond. B, Biol. Sci. 268:2347-2353 (2001).  
DR EMBL; AY012920; AAL31843.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
RN NON TER 1 1  
SQ SEQUENCE 9 AA; 1174 MW; 2B73173B46DDC2D3 CRC64;

Query Match 30.2%; Score 19; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
ID Q9BT05 PRELIMINARY; PRT; 8 AA.  
AC Q9BT05;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update).  
GN Xenopus laevis (African clawed frog).  
OS Xenopus laevis; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN SEQUENCE FROM N.A.  
RP MEDLINE#=21226152; PubMed=11327714;  
RA Nasar P.; Wagnez M.;  
RT "Characterization of two promoters of the Xenopus laevis elrD gene.";  
RL Biochem. Biophys. Res. Commun. 283:392-398 (2001).  
DR EMBL; AF329448; AAK01428.1; -.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 1008 MW; FF9337284537B16 CRC64;

Query Match 28.6%; Score 18; DB 13; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1e-06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
ID Q9RM1 PRELIMINARY; PRT; 9 AA.  
AC Q9RM1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)





OC Daubentonia.  
 OX NCBI\_TaxID=31869;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STREAIN=SP119, and JP120;  
 RX MEDLINE=21184272; Pubmed=11286490;  
 RA Pastori J., Marin R.D., Ehresmann P., Zimmermann B., Forstner M.R.,  
 "Molecular phylogeny of the lemur family Cheirogaleidae (primates)",  
 RT based on mitochondrial DNA sequences.,  
 RL Mol. Phylogenet. Evol. 19:45-56 (2001).  
 DR EMBL; AR224641; ARK70615.1;  
 EMBL; AR224612; ARK70619.1;  
 GO; GO:0005739; C:mitochondrion; IEA.  
 XW Mitochondrion.  
 FT NON TER 1 1 MW; DSC5636365045A2 CRC64;  
 SQ SEQUENCE 9 AA; 1160 MW;

---

Query Match 25.4%; Score 16; DB 8; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OS Tectocoris diophthalmus (cotton harlequin bug).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Bulbipelta; Heteroptera;  
 OC Psylloidea; Pentatomidae; Pentatomidae;  
 OC Tectocoris.  
 OX NCBI\_TaxID=159956;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21396409; PubMed=11504862;  
 RA Shao R., Campbell N.J.H., Schmidt E.R., Barker S.C.;  
 "Increased rate of gene rearrangement in the mitochondrial genomes of  
 three orders of hemipteroid insects.",  
 RL Mol. Biol. Evol. 18:1828-1832 (2001).  
 DR EMBL; AR35990; ARK5283.1;  
 GO; GO:0005739; C:mitochondrion; IEA.  
 XW Mitochondrion.  
 FT NON TER 1 1 MW; A2C5636365041A6 CRC64;  
 SQ SEQUENCE 9 AA; 1206 MW;

---

Query Match 25.4%; Score 16; DB 8; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OS Tectocoris diophthalmus (cotton harlequin bug).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Bulbipelta; Heteroptera;  
 OC Psylloidea; Pentatomidae; Pentatomidae;  
 OC Tectocoris.  
 OX NCBI\_TaxID=159956;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21396409; PubMed=11504862;  
 RA Shao R., Campbell N.J.H., Schmidt E.R., Barker S.C.;  
 "Increased rate of gene rearrangement in the mitochondrial genomes of  
 three orders of hemipteroid insects.",  
 RL Mol. Biol. Evol. 18:1828-1832 (2001).  
 DR EMBL; AR35990; ARK5283.1;  
 GO; GO:0005739; C:mitochondrion; IEA.  
 XW Mitochondrion.  
 FT NON TER 1 1 MW; A2C5636365041A6 CRC64;  
 SQ SEQUENCE 9 AA; 1206 MW;

Search completed: June 1, 2004, 10:28:14  
 Job time : 42 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 10:25:45 ; Search time 54 Seconds  
(without alignments)

47.091 Million cell updates/sec

Title: US-09-756-899A-1

Perfect score: 63

Sequence: 1 AHWGGCCL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 231240

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	9	3 AAY77664	Aay77664 Immunoglobulin
2	63	100.0	9	7 ADC42292	Adc42292 Immunoglobulin
3	36	57.1	8	2 AY21052	Aay21052 Human IgG1
4	35	55.6	8	4 AAB49950	Aab49950 Protein d
5	35	55.6	9	4 AAB49952	Aab49952 Protein d
6	33	52.4	6	4 AAB49951	Aab49951 Protein d
7	33	52.4	6	5 ABP54937	Abp54937 Active site
8	33	52.4	7	2 AAW56315	Aaw56315 Active site
9	32	50.8	7	2 AAY43470	Aay43470 Platypot
10	32	50.8	9	5 AAE19859	Aae19859 TRIP zinc
11	31	49.2	9	4 AAM23018	Aam23018 HIV Peptid
12	31	49.2	9	4 AAU23295	Aau23295 Human MHC
13	31	49.2	9	4 AAU24423	Aau24423 Human MHC
14	30	47.6	9	5 ABB05275	Abb05275 Vascular
15	30	47.6	9	5 ABB05276	Aaw16789 Lamprey I
16	29	46.0	9	2 AAW96789	Aaw16787 Lamprey I
17	29	46.0	9	4 AAB50022	Aab50022 Mutant an
18	29	46.0	9	4 AAB50445	Aab50445 Chymotrypsin
19	28	44.4	8	4 AAB50445	Aar89936 Luteinising hormone
20	28	44.4	9	2 AAW43842	Aaw3842 Specific
21	28	44.4	9	4 AAM22404	Aam22404 HIV peptide
22	28	44.4	9	4 AAM23297	Aam23297 HIV peptide
23	28	44.4	9	4 AAM23021	Aam23021 HIV peptide
24	28	44.4	9	4 AAM23295	Aam23295 HIV peptide
25	28	44.4	9	4 AAM23295	Aam23295 HIV peptide

RESULT 1  
AAV77664 standard; peptide; 9 AA.  
XX  
ID AAV77664  
XX  
AC AAY77664;  
XX  
DT 12-MAY-2000 (first entry)  
XX  
DB Immunoglobulin (Ig) free light chain binding peptide LCBP.  
XX  
Immunoglobulin; Ig; light chain; LC: multiple sclerosis; antiasthmatic;  
KW antiallergy; chronic inflammatory bowel disorder; antiinflammatory;  
KW antiviral; virucide; neuroprotective; antimigraine.  
XX  
Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "N-terminal acetylation"  
FT Modified-site 9 /note= "C-terminal amide"  
XX  
XX  
W020002915-A1.  
XX  
PN W020002915-A1.  
XX  
PT 20-JAN-2000.  
XX  
PT 07-JUL-1999; 99WO-NL000430.  
XX  
PT 09-JUL-1998; 98NL-01009501.  
XX  
PT (UYUT-) RIJKSUNIV Utrecht.  
XX  
PI Redegeld PAM, Kranenfeld AD, Nijkamp FP;  
XX  
DR WPI; 2000-121132/15.  
XX  
New compounds which inhibit immunoglobulin light chain binding to mast cells, used for treating, e.g. asthma.

## CLAIMS

The invention relates to compounds which inhibit the binding of the free light chain (LC) of immunoglobulin (Ig) to mast cells. The compounds can be used for treating e.g. asthma, allergic inflammatory bowel disorders, viral infection or multiple sclerosis, and possibly migraine. The methods can also be used for diagnosing a disease in a patient having an elevated level of the free LC of Ig in a body fluid. The present sequence represents a peptide capable of binding to the free LC of Ig

CC The invention relates to compounds which inhibit the binding of the free light chain (LC) of immunoglobulin (Ig) to mast cells. The compounds can be used for treating e.g. asthma, allergic inflammatory bowel disorders, viral infection or multiple sclerosis, and possibly migraine. The methods can also be used for diagnosing a disease in a patient having an elevated level of the free LC of Ig in a body fluid. The present sequence represents a peptide capable of binding to the free LC of Ig

CC



XX Sequence 8 AA;

SQ Query Match 57.1%; Score 36; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SGFCC 8  
Db 2 SGFCC 6

RESULT 4  
AAB49950 ID AAB49950 standard peptide; 8 AA.  
XX AC AAB49950;  
XX DT 07-MAR-2001 (first entry)  
XX DE Protein disulfide isomerase consensus N-terminus.  
XX Disulphide bond; allergy; protein disulfide isomerase variant; detergent;  
KW food additive; cosmetic.  
OS Mammalia.  
PN WO200070064-A1.  
XX PD 23-NOV-2000.  
XX PF 17-MAY-2000; 2000WO-DK000265.

XX PR 17-MAY-1999; 99DK-00000683.  
XX PR 18-MAY-1999; 99DK-0000689.  
XX PR 02-JUN-1999; 99US-0137068P.  
XX PA (NOVO ) NOVO NORDISK AS.

XX PI Hjort CM;  
XX DR WPI; 2001-070776/08.

XX PT Protein disulfide isomerase variant having increased reducing properties  
PT and decreased redox potential than native proteins, used to reduce  
PT allergenicity of allergic proteins in feed, food or cosmetic products.

XX Example 1; Page 33; 82pp; English.

XX PS 23-NOV-2000.  
XX PF 17-MAY-2000; 2000WO-DK000265.  
XX PR 17-MAY-1999; 99DK-00000683.  
XX PR 18-MAY-1999; 99DK-0000689.  
XX PR 02-JUN-1999; 99US-0137068P.  
XX PA (NOVO ) NOVO NORDISK AS.

XX PI Hjort CM;  
XX DR WPI; 2001-070776/08.

XX PT Protein disulfide isomerase variant having increased reducing properties  
PT and decreased redox potential than native proteins, used to reduce  
PT allergenicity of allergic proteins in feed, food or cosmetic products.

XX Example 1; Page 33; 82pp; English.

XX PS 23-NOV-2000.  
XX CC The present invention provides variants of the Aspergillus oryzae protein  
CC disulfide isomerase enzyme. These are capable of reducing disulphide  
CC bonds in proteins, which may be the cause of allergies in humans. The  
CC proteins can be used to reduce the allergenicity of foods, to treat  
CC scleroproteins, in detergents, in food additives and in cosmetics

XX SQ Sequence 9 AA;  
Query Match 55.6%; Score 35; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AHWSGHC 7  
Db 2 APWCGHC 8

RESULT 6  
AAB49951 ID AAB49951 standard; peptide; 6 AA.  
XX AC AAB49951;  
XX DT 07-MAR-2001 (first entry)

XX DE Protein disulfide isomerase consensus N-terminus.

XX KW Disulphide bond; allergy; protein disulfide isomerase variant; detergent;  
KW food additive; cosmetic.

XX OS Mammalia.  
PN WO200070064-A1.  
XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-DK000265.

XX PR 17-MAY-1999; 99DK-00000683.  
XX PR 18-MAY-1999; 99DK-0000689.  
XX PR 02-JUN-1999; 99US-0137068P.  
XX PA (NOVO ) NOVO NORDISK AS.

RESULT 5  
AAB49952 ID AAB49952 standard; peptide; 9 AA.  
XX AC AAB49952;  
XX DT 07-MAR-2001 (first entry)

XX Hjort GM;  
 PI  
 XX WPI; 2001-070776/08.  
 Protein disulfide isomerase variant having increased reducing properties and decreased redox potential than native proteins, used to reduce allergenicity of allergic proteins in food, food or cosmetic products.  
 Example 1; Page 33; 82PP; English.  
 XX  
 CC The present invention provides variants of the Aspergillus oryzae protein disulfide isomerase enzyme. These are capable of reducing disulfide bonds in proteins, which may be the cause of allergies in humans. The proteins can be used to reduce the allergenicity of foods, to treat scleroproteins, in detergents, in food additives and in cosmetics.  
 XX Sequence 6 AA;

Query Match 52.4%; Score 33; DB 4; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 4; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSGHC 7  
 Db 1 WCGHC 5

Sequence 6 AA;

Qy	3 WSGHC 7	RESULT 9	XX	AAE19859 standard; peptide; 9 AA.
Db	2 WCGHC 6	AAV43470	ID AAE19859;	AAE19859 standard; peptide; 9 AA.
		ID AAV43470 standard; peptide; 7 AA.	AC	AAE19859;
		XX	AC	AAE19859;
		XX	DT	18-JUN-2002 (first entry)
		XX	DE	TRIP zinc finger domain consensus.
		XX	XX	Human; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
		XX	XX	TNF; TNF receptor; TRIP; cell activation; cell proliferation;
		XX	XX	cell death; therapy; cytosstatic; zinc finger domain.
		XX	OS	Homo sapiens.
		OS	OS	Mus sp.
		OS	PN	US6346605-B1.
		OS	XX	US6346605-B1.
		PN	XX	12-FEB-2002.
		PN	XX	98US-00052889.
		XX	PF	31-MAR-1998;
		XX	XX	98US-00052889.
		PD	PR	01-APR-1997;
		XX	PR	97US-0042293P.
		XX	PR	07-APR-1997;
		XX	XX	97US-0042747P.
		XX	PA	(UTRQ ) UNIV ROCKEFELLER.
		XX	XX	PT
		XX	PT	New tumor necrosis factor receptor associated factor interacting protein.
		XX	PT	PT useful for inhibiting NF-kappa B activation, and for modulating signals
		XX	PT	responsible for cell activation, cell proliferation, and cell death.
		XX	XX	Example 2: Fig 2D; 37PP; English.
		XX	XX	The present invention relates to a tumour necrosis factor (TNF) receptor
		XX	CC	associated factor (TRAF) interacting protein (TRIP), which is a regulator
		XX	CC	capable of binding to TRAF2. TRIP is useful for inhibiting NF-kappa B
		XX	CC	activation, and for modulating signals responsible for cell activation,
		XX	CC	cell proliferation, and cell death. Thus, TRIP is useful for treating
		XX	CC	diseases associated with altered cell proliferation and cell death. The
		XX	CC	present sequence is zinc finger domain consensus sequence of human and
		XX	CC	mouse TRIP
		XX	CC	Sequence 9 AA:
		XX	CC	Query Match Score 32; DB 5; Length 9;
		XX	CC	Best Local Similarity 100.0%; Pred. No. 1.4e+06;
		XX	CC	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		XX	Qy	5 GHCC 8
		XX	DB	4 GHCC 7
		XX	XX	RESULT 11
		XX	AC	AAM23018
		XX	XX	22-OCT-2001 (first entry)
		XX	XX	HIV peptide SEQ ID NO 903.
		XX	DB	Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
		XX	KW	human immunodeficiency virus; vaccine.
SQ	3 WSGHCC 8	Qy	3 WSGHCC 8	3 WSGHCC 8
	2 WCGHCC 7	Db	2 WCGHCC 7	2 WCGHCC 7

OS Human immunodeficiency virus.

OS Synthetic.

XX WO200155177-A2.

XX PD 02-AUG-2001.

XX PP 29-JAN-2001; 2001WO-DK0000059.

XX PR 28-JAN-2000; 2000EP-00610017.

XX PR 31-JAN-2000; 2000US-0179333P.

XX (STATS-) STATENS SERUM INST.

XX PI Fomsgaard A, Brunak S, Buus S, Corbet S, Latemoller SP, Hansen J;

XX DR; 2001-476184/51.

XX PS Example 4; Page 70; 383pp; English.

The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAW22116 AAW23484) that generate anti-HIV activity.

CC are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents

CC SQ Sequence 9 AA;

CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAW22116 AAW23484) that generate anti-HIV activity.

CC are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents

CC SQ Sequence 9 AA;

CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAW22116 AAW23484) that generate anti-HIV activity.

CC are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents

CC SQ Sequence 9 AA;

CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAW22116 AAW23484) that generate anti-HIV activity.

CC are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents

CC SQ Sequence 9 AA;

CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAW22116 AAW23484) that generate anti-HIV activity.

CC are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents

CC SQ Sequence 9 AA;

CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAW22116 AAW23484) that generate anti-HIV activity.

CC are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents

CC SQ Sequence 9 AA;

CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAW22116 AAW23484) that generate anti-HIV activity.

CC are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents

CC SQ Sequence 9 AA;

CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAW22116 AAW23484) that generate anti-HIV activity.

CC are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents

CC SQ Sequence 9 AA;

CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAW22116 AAW23484) that generate anti-HIV activity.

CC are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents

DR WPI; 2001-557705/62.

XX New polynucleotide for treating and diagnosing prostate cancer is the 103P2D6 gene which encodes for 103P2D6-related proteins.

XX Example 15; Page 81; 132pp; English.

XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and peptide fragments of the polypeptide. 103P2D6 is not expressed in normal adult tissue but is aberrantly expressed in some foetal tissues and many cancers including tumours of the prostate, testis, bladder, bone, cervix, ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its related protein and also peptide fragments of the protein are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 103P2D6-related protein, and a ribozyme capable of cleaving a polynucleotide having the 103P2D6 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P2D6. The sequences can be used in diagnostic methods to monitor the level of 103P2D6 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 9 AA;

CC Query Match 49.2%; Score 31; DB 4; Length 9;

CC Best Local Similarity 57.1%; Pred. No. 1.4e+06; Mismatches 1; Indels 0; Gaps 0;

CC Matches 5; Conservative 0; MisMatches 2; Indels 0; Gaps 0;

CC Qy 3 WSGHCCL 9

CC Db 1 WSGRCGL 7

CC XX RESULT 13

CC ID AAU24423 standard; peptide: 9 AA.

CC AC AAU24423;

CC XX DT 17-DEC-2001 (first entry)

CC DB Human MHC molecule HLA-B35 binding 103P2D6 peptide #8.

CC XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;

CC KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;

CC KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;

CC KW single chain monoclonal antibody; cervix; human.

CC XX Homo sapiens.

CC XX PA (UROG-) UROGENEWS INC.

CC XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;

CC PI Challita-Eid PM, Faris M, Jakobovits A;

CC XX PR (UROG-) UROGENEWS INC.

CC XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;

CC PI Challita-Eid PM, Faris M, Jakobovits A;

CC XX DR 2001-557705/62.

CC PT New polynucleotide for treating and diagnosing prostate cancer is the 103P2D6 gene which encodes for 103P2D6-related proteins.

CC XX Example 15; Page 97; 132pp; English.

CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and

CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal

CC adult tissue but is aberrantly expressed in some foetal tissues and many

CC cancers including tumours of the prostate, testis, bladder, bone, cervix,

CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its

CC related protein and also peptide fragments of the protein are therefore

CC useful for diagnosing and treating cancer. A vector comprising a

CC polynucleotide which encodes a single chain monoclonal antibody, that

CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme

CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,

CC are both useful in the preparation of a composition for treating a

CC patient with a cancer that expresses 103P2D6. The sequences can be used

CC in diagnostic methods to monitor the level of 103P2D6 gene products in

CC serum, blood, urine and tissue and to thereby detect the presence of

CC cancerous cells.

peptide fragments of the polypeptide, 103P2D6 is not expressed in normal adult tissue but is aberrantly expressed in some foetal tissues and many cancers including tumours of the prostate, testis, bladder, bone, cervix, ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its related protein and also peptide fragments of the protein are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 103P2D6-related protein, and a ribozyme capable of cleaving a polynucleotide having the 103P2D6 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P2D6. The sequences can be used in diagnostic methods to monitor the level of 103P2D6 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

Sequence 9 AA;

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

Query Match 49.2%; Score 31; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06; Gaps 0;

Matches 5; Conservative 2; Indels 0; Gaps 0;

Qy 3 WSGHCCU 9  
Db 1 WSSRCGL 7

capable of cleaving a polynucleotide having the 103P2D6 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P2D6. The sequences can be used in diagnostic methods to monitor the level of 103P2D6 Gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

Sequence 9 AA;

Query Match 47.6%; Score 30; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

SQ XX  
SQ Sequence 9 AA;

Query Match 47.6%; Score 30; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

SQ XX  
SQ Sequence 9 AA;

RESULT 15  
ID AAU24453 standard; peptide; 9 AA.

ID AAU24453; peptide; 9 AA.

ID AAU2445

CC human body stain, to allow unbound peptide to bind with the stain to form  
CC stain-bound peptide complex and identifying the stain-bound peptide on  
CC the stain-bound peptide complex. A selective targeting method for  
CC screening a library of ligands that bind to a target may be used to  
CC identify ligands that bind to a target under harsh conditions. The  
CC selective targeting method may be used to screen and identify a ligand  
CC useful for therapeutic intervention, e.g., a library of ligands may be  
CC screened to identify a tumour-bound ligand. The selective targeting  
CC method may be used to identify cell type specific surface molecules.  
CC Preferred anti-targets include one or more different cell types, cells in  
CC different states, or cells that do not display the surface molecule.  
CC ABB0232 to ABB05346 represent phage-peptides ligands which are used in  
CC the exemplification of the present invention. (Updated on 29-AUG-2003 to  
CC standardise OS field)

XX Sequence 9 AA;

Query Match 47.6%; Score 30; DB 5; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 AHWSGHCC 8  
| : | |  
Db 2 APWNSHIC 9

Search completed: June 1, 2004, 10:26:56  
Job time : 56 secs



APPLICANT: Lee, Frank D.  
 APPLICANT: Meng, Dr. Xun  
 APPLICANT: Chan, John W.  
 APPLICANT: Zhang, Shengsheng J.  
 APPLICANT: Benkovic, Stephen J.  
 TITLE OF INVENTION: PROTEIN ANALYSIS  
 FILE REFERENCE: ENE-E01-001  
 CURRENT FILING DATE: 2003-05-12  
 PRIOR APPLICATION NUMBER: 60/379,626  
 PRIOR FILING DATE: 2002-05-10  
 PRIOR APPLICATION NUMBER: 60/393,233  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,235  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,212  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,280  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,197  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,223  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/430,948  
 PRIOR FILING DATE: 2003-12-04  
 PRIOR APPLICATION NUMBER: 60/433,319  
 PRIOR FILING DATE: 2002-12-13  
 PRIOR APPLICATION NUMBER: 60/393,137  
 PRIOR FILING DATE: 2002-07-01  
 NUMBER OF SEQ ID NOS: 614  
 SEQ ID NO: 494  
 LENGTH: 5  
 TYPE: PRT  
 ORGANISM: Human  
 US-10-436-549-494

Query Match Score 57.1%; Best Local Similarity 100.0%; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Organism: homo sapiens

RESULT 3  
 US-09-793-451-52  
 / Sequence 52, Application US/09793451  
 / Publication No. US20030157597A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Arthur B. Raitano  
 / APPLICANT: Daniel B. Afar  
 / APPLICANT: Gazelle S. Rastegar  
 / APPLICANT: Steve Chappell Mitchell  
 / APPLICANT: Rene S. Hubert  
 / APPLICANT: Pia M. Challita-Bid  
 / APPLICANT: Mary Paris  
 / APPLICANT: Aya Jakobovits  
 / APPLICANT: Ayia Jakobovits  
 / APPLICANT: Mary Paris  
 / TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY EXPRESSED IN VARIOUS CANCERS  
 / FILE REFERENCE: 129 .2USU2  
 / CURRENT APPLICATION NUMBER: US/09/793,451  
 / CURRENT FILING DATE: 2003-04-10  
 / PRIOR APPLICATION NUMBER: PCT/DK01/00059  
 / PRIOR FILING DATE: 2001-01-29  
 / PRIOR APPLICATION NUMBER: EP 00610017-6  
 / PRIOR FILING DATE: 2000-01-28  
 / PRIOR APPLICATION NUMBER: US 60/179,333

SEQ ID NO: 52  
 LENGTH: 9

Qy 5 GHCL 9  
 Db 1 GHCCCL 5

Query Match Score 36%; Best Local Similarity 100.0%; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Organism: homo sapiens

RESULT 4  
 US-09-793-451-622  
 / Sequence 622, Application US/09793451  
 / Publication No. US20030157597A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Arthur B. Raitano  
 / APPLICANT: Daniel B. Afar  
 / APPLICANT: Gazelle S. Rastegar  
 / APPLICANT: Steve Chappell Mitchell  
 / APPLICANT: Rene S. Hubert  
 / APPLICANT: Pia M. Challita-Bid  
 / APPLICANT: Mary Paris  
 / APPLICANT: Aya Jakobovits  
 / APPLICANT: Ayia Jakobovits  
 / APPLICANT: Mary Paris  
 / TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY EXPRESSED IN VARIOUS CANCERS  
 / FILE REFERENCE: 129 .2USU2  
 / CURRENT APPLICATION NUMBER: US/09/793,451  
 / CURRENT FILING DATE: 2001-02-26  
 / PRIOR APPLICATION NUMBER: 60/184,558  
 / PRIOR FILING DATE: 2000-02-24  
 / PRIOR APPLICATION NUMBER: 60/218,856  
 / PRIOR FILING DATE: 2000-07-13  
 / NUMBER OF SEQ ID NOS: 732  
 / SOFTWARE: FastSBQ for Windows Version 4.0  
 / SEQ ID NO: 622  
 / LENGTH: 9  
 / TYPE: PRT  
 / ORGANISM: homo sapiens  
 / US-09-793-451-622

Qy 3 WSGHCL 9  
 Db 1 WSGRGL 7

Query Match Score 31%; Best Local Similarity 71.4%; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Organism: homo sapiens

RESULT 5  
 US-10-18-252A-903  
 / Sequence 903, Application US/10182252A  
 / Publication No. US20040072162A1  
 / GENERAL INFORMATION:  
 / APPLICANT: FOMAGARD, ANDERS  
 / APPLICANT: BRUNAK, SOREN  
 / APPLICANT: BUDS, SOREN  
 / APPLICANT: CORBET, SYLVIE  
 / APPLICANT: LAUTEMOLLER, SANNE LISE  
 / TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND CONTROL OF HIV INFECTIONS  
 / FILE REFERENCE: 030107/0205  
 / CURRENT APPLICATION NUMBER: US/10/182,252A  
 / CURRENT FILING DATE: 2003-04-10  
 / PRIOR APPLICATION NUMBER: PCT/DK01/00059  
 / PRIOR FILING DATE: 2001-01-29  
 / PRIOR APPLICATION NUMBER: EP 00610017-6  
 / PRIOR FILING DATE: 2000-01-28  
 / PRIOR APPLICATION NUMBER: US 60/179,333

SEQ ID NO: 52  
 LENGTH: 9

Qy 3 WSGHCL 9  
 Db 1 WSGRGL 7

Query Match Score 31%; Best Local Similarity 71.4%; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Organism: homo sapiens

```

; PRIORITY FILING DATE: 2000-01-31
; TITLE OF INVENTION: 103P2D6 : TISSUE SPECIFIC PROTEIN HIGHLY
; EXPRESSED IN VARIOUS CANCERS
; SEQ ID NO: 903
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
; US-10-182-052-A-903
Query Match 49.2%; Score 31; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Software: FastSEQ for Windows Version 4.0
SEQ ID NO: 622
Length: 9
TYPE: PRT
ORGANISM: homo sapiens
US-10-283-722-622

RESULT 6
US-10-283-722-52
Sequence 52, Application US/10283722
Publication No. US20030194407A1
GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; APPLICANT: Rene S. Hubert Mitchell
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.ZUSU2
; CURRENT APPLICATION NUMBER: US/10/283.722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; SEQ ID NO: 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-52

Query Match 49.2%; Score 31; DB 14; Length 9;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Software: FastSEQ for Windows Version 4.0
SEQ ID NO: 52
Length: 9
TYPE: PRT
ORGANISM: homo sapiens
US-10-283-903-52

RESULT 7
US-10-283-722-622
Sequence 622, Application US/10283722
Publication No. US20030194407A1
GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; APPLICANT: Rene S. Hubert Mitchell
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.ZUSU2
; CURRENT APPLICATION NUMBER: US/10/283.903
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; SEQ ID NO: 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-622

Query Match 49.2%; Score 31; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Software: FastSEQ for Windows Version 4.0
SEQ ID NO: 52
Length: 9
TYPE: PRT
ORGANISM: homo sapiens
US-10-283-903-52

RESULT 9
US-10-283-903-622
Sequence 622, Application US/10283903
Publication No. US20030194407A1
GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; APPLICANT: Rene S. Hubert Mitchell
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.ZUSU2
; CURRENT APPLICATION NUMBER: US/10/283.903
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; SEQ ID NO: 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-903-622

```

Publication No. US20030219766A1  
 GENERAL INFORMATION:  
 APPLICANT: Arthur B. Raitano  
 APPLICANT: Daniel P.H. Afar  
 APPLICANT: Gazelle S. Rascollar  
 APPLICANT: Steve Chappell Mitchell  
 APPLICANT: Rene S. Hubert  
 APPLICANT: Pia M. Challita-Bid  
 APPLICANT: Mary Faris  
 APPLICANT: Aya Jakobovits  
 TITLE OF INVENTION: 103PDD6: TISSUE SPECIFIC PROTEIN HIGHLY EXPRESSED IN VARICOS CANCERS  
 FILE REFERENCE: 129 2USU2  
 CURRENT APPLICATION NUMBER: US/10/283,903  
 CURRENT FILING DATE: 2003-02-03  
 PRIOR APPLICATION NUMBER: US/09/793,451  
 PRIOR FILING DATE: 2001-02-26  
 PRIOR APPLICATION NUMBER: 60/184,558  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: 60/218,856  
 PRIOR FILING DATE: 2000-07-13  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 622  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-10-283-903-622

Query Match 31; Score: 49.2%; Best Local Similarity: 71.4%; Matches: 5; Conservative: 0; Indels: 2; NOS: 0;  
 Qy 3 WSGHCL 9  
 Db 1 WSGRGL 7

RESULT 10  
 US-10-436-549-497  
 Sequence 497, Application US/10436549  
 Publication No. US20040038207A1  
 GENERAL INFORMATION:  
 APPLICANT: Lee, Frank D.  
 APPLICANT: Meng, Dr. Kun  
 APPLICANT: Chan, John W.  
 APPLICANT: Zhang, Shengsheng  
 APPLICANT: Penkovic, Stephen J.  
 TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN  
 FILE REFERENCE: ENGE-P01-001  
 CURRENT APPLICATION NUMBER: US/10/436,549  
 CURRENT FILING DATE: 2003-05-12  
 PRIOR APPLICATION NUMBER: 60/379,626  
 PRIOR FILING DATE: 2002-07-10  
 PRIOR APPLICATION NUMBER: 60/393,233  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,235  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,211  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,280  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,197  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/393,223  
 PRIOR FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/430,948  
 PRIOR FILING DATE: 2002-12-04  
 PRIOR APPLICATION NUMBER: 60/432,319  
 PRIOR FILING DATE: 2002-12-13  
 PRIOR APPLICATION NUMBER: 60/393,137  
 PRIOR FILING DATE: 2002-07-01

RESULT 11  
 US-09-832-723-108  
 Sequence 108, Application US/09832723  
 Patent No. US20020098524A1  
 GENERAL INFORMATION:  
 APPLICANT: Batelli, David A.  
 APPLICANT: Chen, Yiyou  
 APPLICANT: Murray, Christopher J.  
 APPLICANT: Tijerina, Pilata  
 TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
 FILE REFERENCE: GO617-2  
 CURRENT APPLICATION NUMBER: US/09/832,723  
 CURRENT FILING DATE: 2001-04-11  
 PRIOR APPLICATION NUMBER: US 60/197,259  
 PRIOR FILING DATE: 2000-04-14  
 NUMBER OF SEQ ID NOS: 117  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 108  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: peptides screened from a phage display random peptide library  
 US-09-832-723-108

Query Match 31; Score: 47.6%; Best Local Similarity: 50.0%; Matches: 4; Conservative: 1; Indels: 3; NOS: 0;  
 Qy 1 AHNSHCC 8  
 Db 2 APNNSHIC 9

RESULT 12  
 US-09-793-451-652  
 Sequence 652, Application US/09793451  
 Publication No. US20030157597A1  
 GENERAL INFORMATION:  
 APPLICANT: Arthur B. Raitano  
 APPLICANT: Daniel E.H. Afar  
 APPLICANT: Gazelle S. Rastegar  
 APPLICANT: Steve Chappell Mitchell  
 APPLICANT: Rene S. Hubert  
 APPLICANT: Pia M. Challita-Bid  
 APPLICANT: Mary Faris  
 APPLICANT: Aya Jakobovits  
 TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY EXPRESSED IN VARIOUS CANCERS  
 FILE REFERENCE: 129 2USU2  
 CURRENT APPLICATION NUMBER: US/09/793,451  
 CURRENT FILING DATE: 2001-02-26  
 PRIOR APPLICATION NUMBER: 60/184,558  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: 60/218,856  
 PRIOR FILING DATE: 2000-07-01  
 PRIOR APPLICATION NUMBER: 60/218,856

```

; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 652
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-652

Query Match Score 30; DB 14; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Software: FastSEQ for Windows Version 4.0
SEQ ID NO: 652
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-652

Qy 3 WSGHC 7
Db 5 WSGRC 9

RESULT 13
US-10-303-331-108
; Sequence 108, Application US/10303331
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; MURRAY, Christopher J.
; APPLICANT: Winetzyk, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETTING
; FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-10-303-331-108

Query Match Score 30; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Software: FastSEQ for Windows Version 4.0
SEQ ID NO: 652
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-903-652

RESULT 14
US-10-283-722-652
; Sequence 652, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129 2USU2
; CURRENT APPLICATION NUMBER: US/10/283,903
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 652
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-903-652

Query Match Score 30; DB 14; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Software: FastSEQ for Windows Version 4.0
SEQ ID NO: 652
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-903-652

Search completed: June 1, 2004, 10:33:57
Job time : 43 secs

```